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Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=11; day=12; hr=14; min=10; sec=53; ms=629;  
]

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Application No: 10589381

Version No: 2.0

Input Set:

Output Set:

Started: 2008-10-20 12:44:09.709

Finished: 2008-10-20 12:44:11.266

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 557 ms

Total Warnings: 20

Total Errors: 0

No. of SeqIDs Defined: 20

Actual SeqID Count: 20

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 402	Undefined organism found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
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W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)



# SEQUENCE LISTING

<110> Anderson, Annaliesa S.  
Montgomery, Donna L.

<120> POLYPEPTIDES FOR INDUCING A PROTECTIVE  
IMMUNE RESPONSE AGAINST STAPHYLOCOCCUS AUREUS

<130> 21490YP

<140> 10589381

<141> 2006-08-15

<150> PCT/US2005/004431

<151> 2005-02-14

<150> 60/545,447

<151> 2004-02-18

<160> 20

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 260

<212> PRT

<213> Artificial Sequence

<220>

<223> truncated derivative of sai-1

<400> 1

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Val	Gln	Lys	Asp	Gly	Ser	Ser	Glu	Lys	Ser	His	Met	Asp	Asp	Tyr	Met
			20					25					30		
Gln	His	Pro	Gly	Lys	Val	Ile	Lys	Gln	Asn	Asn	Lys	Tyr	Tyr	Phe	Gln
		35					40					45			
Thr	Val	Leu	Asn	Asn	Ala	Ser	Phe	Trp	Lys	Glu	Tyr	Lys	Phe	Tyr	Asn
		50				55					60				
Ala	Asn	Asn	Gln	Glu	Leu	Ala	Thr	Thr	Val	Val	Asn	Asp	Asn	Lys	Lys
65					70					75				80	
Ala	Asp	Thr	Arg	Thr	Ile	Asn	Val	Ala	Val	Glu	Pro	Gly	Tyr	Lys	Ser
			85						90				95		
Leu	Thr	Thr	Lys	Val	His	Ile	Val	Val	Pro	Gln	Ile	Asn	Tyr	Asn	His
			100					105					110		
Arg	Tyr	Thr	Thr	His	Leu	Glu	Phe	Glu	Lys	Ala	Ile	Pro	Thr	Leu	Ala
		115					120					125			
Asp	Ala	Ala	Lys	Pro	Asn	Asn	Val	Lys	Pro	Val	Gln	Pro	Lys	Pro	Ala
		130				135					140				
Gln	Pro	Lys	Thr	Pro	Thr	Glu	Gln	Thr	Lys	Pro	Val	Gln	Pro	Lys	Val
145					150					155				160	
Glu	Lys	Val	Lys	Pro	Thr	Val	Thr	Thr	Thr	Ser	Lys	Val	Glu	Asp	Asn
					165				170					175	



<210> 3  
<211> 280  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> amino His-tagged construct of SEQ ID NO: 1

<400> 3  
Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
1 5 10 15  
Arg Gly Ser His Met Gly Thr Gln Val Ser Gln Ala Thr Ser Gln Pro  
20 25 30  
Ile Asn Phe Gln Val Gln Lys Asp Gly Ser Ser Glu Lys Ser His Met  
35 40 45  
Asp Asp Tyr Met Gln His Pro Gly Lys Val Ile Lys Gln Asn Asn Lys  
50 55 60  
Tyr Tyr Phe Gln Thr Val Leu Asn Asn Ala Ser Phe Trp Lys Glu Tyr  
65 70 75 80  
Lys Phe Tyr Asn Ala Asn Asn Gln Glu Leu Ala Thr Thr Val Val Asn  
85 90 95  
Asp Asn Lys Lys Ala Asp Thr Arg Thr Ile Asn Val Ala Val Glu Pro  
100 105 110  
Gly Tyr Lys Ser Leu Thr Thr Lys Val His Ile Val Val Pro Gln Ile  
115 120 125  
Asn Tyr Asn His Arg Tyr Thr Thr His Leu Glu Phe Glu Lys Ala Ile  
130 135 140  
Pro Thr Leu Ala Asp Ala Ala Lys Pro Asn Asn Val Lys Pro Val Gln  
145 150 155 160  
Pro Lys Pro Ala Gln Pro Lys Thr Pro Thr Glu Gln Thr Lys Pro Val  
165 170 175  
Gln Pro Lys Val Glu Lys Val Lys Pro Thr Val Thr Thr Thr Ser Lys  
180 185 190  
Val Glu Asp Asn His Ser Thr Lys Val Val Ser Thr Asp Thr Thr Lys  
195 200 205  
Asp Gln Thr Lys Thr Gln Thr Ala His Thr Val Lys Thr Ala Gln Thr  
210 215 220  
Ala Gln Glu Gln Asn Lys Val Gln Thr Pro Val Lys Asp Val Ala Thr  
225 230 235 240  
Ala Lys Ser Glu Ser Asn Asn Gln Ala Val Ser Asp Asn Lys Ser Gln  
245 250 255  
Gln Thr Asn Lys Val Thr Lys His Asn Glu Thr Pro Lys Gln Ala Ser  
260 265 270  
Lys Ala Lys Glu Leu Pro Lys Thr  
275 280

<210> 4  
<211> 284  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> amino His-tagged construct of SEQ ID NO: 2

<400> 4

Met	Gly	Ser	Ser	His	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro
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Arg	Gly	Ser	His	Met	Gly	Thr	Gln	Val	Ser	Gln	Ala	Thr	Ser	Gln	Pro
			20					25						30	
Ile	Asn	Phe	Gln	Val	Gln	Lys	Asp	Gly	Ser	Ser	Glu	Lys	Ser	His	Met
	35					40					45				
Asp	Asp	Tyr	Met	Gln	His	Pro	Gly	Lys	Val	Ile	Lys	Gln	Asn	Asn	Lys
	50					55					60				
Tyr	Tyr	Phe	Gln	Ala	Val	Leu	Asn	Asn	Ala	Ser	Phe	Trp	Lys	Glu	Tyr
65					70					75					80
Lys	Phe	Tyr	Asn	Ala	Asn	Asn	Gln	Glu	Leu	Ala	Thr	Thr	Val	Val	Asn
				85					90					95	
Asp	Asp	Lys	Lys	Ala	Asp	Thr	Arg	Thr	Ile	Asn	Val	Ala	Val	Glu	Pro
		100						105					110		
Gly	Tyr	Lys	Ser	Leu	Thr	Thr	Lys	Val	His	Ile	Val	Val	Pro	Gln	Ile
	115						120					125			
Asn	Tyr	Asn	His	Arg	Tyr	Thr	Thr	His	Leu	Glu	Phe	Glu	Lys	Ala	Ile
	130					135					140				
Pro	Thr	Leu	Ala	Asp	Ala	Ala	Lys	Pro	Asn	Asn	Val	Lys	Pro	Val	Gln
145					150					155					160
Pro	Lys	Pro	Ala	Gln	Pro	Lys	Thr	Pro	Thr	Glu	Gln	Thr	Lys	Pro	Val
				165					170					175	
Gln	Pro	Lys	Val	Glu	Lys	Val	Lys	Pro	Ala	Val	Thr	Ala	Pro	Ser	Lys
		180						185					190		
Asn	Glu	Asn	Arg	Gln	Thr	Thr	Lys	Val	Val	Ser	Ser	Glu	Ala	Thr	Lys
	195						200					205			
Asp	Gln	Ser	Gln	Thr	Gln	Ser	Ala	Arg	Thr	Val	Lys	Thr	Thr	Gln	Thr
	210					215					220				
Ala	Gln	Asp	Gln	Asn	Lys	Val	Gln	Thr	Pro	Val	Lys	Asp	Val	Ala	Thr
225					230					235					240
Ala	Lys	Ser	Glu	Ser	Asn	Asn	Gln	Ala	Val	Ser	Asp	Asn	Lys	Ser	Gln
				245					250					255	
Gln	Thr	Asn	Lys	Val	Thr	Lys	Gln	Asn	Glu	Val	His	Lys	Gln	Gly	Pro
		260						265					270		
Ser	Lys	Asp	Ser	Lys	Ala	Lys	Glu	Leu	Pro	Lys	Thr				
	275							280							

<210> 5

<211> 268

<212> PRT

<213> Artificial Sequence

<220>

<223> carboxyl His-tagged construct of SEQ ID NO: 1

<400> 5

Met	Gly	Thr	Gln	Val	Ser	Gln	Ala	Thr	Ser	Gln	Pro	Ile	Asn	Phe	Gln
1				5					10					15	
Val	Gln	Lys	Asp	Gly	Ser	Ser	Glu	Lys	Ser	His	Met	Asp	Asp	Tyr	Met
		20						25					30		
Gln	His	Pro	Gly	Lys	Val	Ile	Lys	Gln	Asn	Asn	Lys	Tyr	Tyr	Phe	Gln
	35						40					45			
Thr	Val	Leu	Asn	Asn	Ala	Ser	Phe	Trp	Lys	Glu	Tyr	Lys	Phe	Tyr	Asn
	50					55					60				
Ala	Asn	Asn	Gln	Glu	Leu	Ala	Thr	Thr	Val	Val	Asn	Asp	Asn	Lys	Lys
65					70					75					80

Ala	Asp	Thr	Arg	Thr	Ile	Asn	Val	Ala	Val	Glu	Pro	Gly	Tyr	Lys	Ser		
				85					90					95			
Leu	Thr	Thr	Lys	Val	His	Ile	Val	Val	Pro	Gln	Ile	Asn	Tyr	Asn	His		
			100					105					110				
Arg	Tyr	Thr	Thr	His	Leu	Glu	Phe	Glu	Lys	Ala	Ile	Pro	Thr	Leu	Ala		
		115					120					125					
Asp	Ala	Ala	Lys	Pro	Asn	Asn	Val	Lys	Pro	Val	Gln	Pro	Lys	Pro	Ala		
	130					135					140						
Gln	Pro	Lys	Thr	Pro	Thr	Glu	Gln	Thr	Lys	Pro	Val	Gln	Pro	Lys	Val		
145					150				155					160			
Glu	Lys	Val	Lys	Pro	Thr	Val	Thr	Thr	Thr	Ser	Lys	Val	Glu	Asp	Asn		
			165					170					175				
His	Ser	Thr	Lys	Val	Val	Ser	Thr	Asp	Thr	Thr	Lys	Asp	Gln	Thr	Lys		
		180						185				190					
Thr	Gln	Thr	Ala	His	Thr	Val	Lys	Thr	Ala	Gln	Thr	Ala	Gln	Glu	Gln		
	195					200				205							
Asn	Lys	Val	Gln	Thr	Pro	Val	Lys	Asp	Val	Ala	Thr	Ala	Lys	Ser	Glu		
	210					215				220							
Ser	Asn	Asn	Gln	Ala	Val	Ser	Asp	Asn	Lys	Ser	Gln	Gln	Thr	Asn	Lys		
225					230					235				240			
Val	Thr	Lys	His	Asn	Glu	Thr	Pro	Lys	Gln	Ala	Ser	Lys	Ala	Lys	Glu		
			245						250				255				
Leu	Pro	Lys	Thr	Leu	Glu	His	His	His	His	His	His						
		260						265									

<210> 6

<211> 395

<212> PRT

<213> Artificial Sequence

<220>

<223> amino His-tagged construct of SEQ ID NO: 7

<400> 6

Met	His	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro	Arg	Gly	Ser		
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Gly	Met	Lys	Glu	Thr	Ala	Ala	Ala	Lys	Phe	Glu	Arg	Gln	His	Met	Asp		
		20						25					30				
Ser	Pro	Asp	Leu	Gly	Thr	Asp	Asp	Asp	Asp	Lys	Ala	Met	Gly	Thr	Lys		
	35					40						45					
His	Tyr	Leu	Asn	Ser	Lys	Tyr	Gln	Ser	Glu	Gln	Arg	Ser	Ser	Ala	Met		
	50				55						60						
Lys	Lys	Ile	Thr	Met	Gly	Thr	Ala	Ser	Ile	Ile	Leu	Gly	Ser	Leu	Val		
65				70					75					80			
Tyr	Ile	Gly	Ala	Asp	Ser	Gln	Gln	Val	Asn	Ala	Ala	Thr	Glu	Ala	Thr		
			85					90					95				
Asn	Ala	Thr	Asn	Asn	Gln	Ser	Thr	Gln	Val	Ser	Gln	Ala	Thr	Ser	Gln		
	100							105					110				
Pro	Ile	Asn	Phe	Gln	Val	Gln	Lys	Asp	Gly	Ser	Ser	Glu	Lys	Ser	His		
	115						120					125					
Met	Asp	Asp	Tyr	Met	Gln	His	Pro	Gly	Lys	Val	Ile	Lys	Gln	Asn	Asn		
	130				135						140						
Lys	Tyr	Tyr	Phe	Gln	Thr	Val	Leu	Asn	Asn	Ala	Ser	Phe	Trp	Lys	Glu		
145				150						155				160			
Tyr	Lys	Phe	Tyr	Asn	Ala	Asn	Asn	Gln	Glu	Leu	Ala	Thr	Thr	Val	Val		
			165					170					175				



Asn	Asp	Asn	Lys	Lys	Ala	Asp	Thr	Arg	Thr	Ile	Asn	Val	Ala	Val	Glu
			180					185					190		
Pro	Gly	Tyr	Lys	Ser	Leu	Thr	Thr	Lys	Val	His	Ile	Val	Val	Pro	Gln
		195					200					205			
Ile	Asn	Tyr	Asn	His	Arg	Tyr	Thr	Thr	His	Leu	Glu	Phe	Glu	Lys	Ala
	210				215					220					
Ile	Pro	Thr	Leu	Ala	Asp	Ala	Ala	Lys	Pro	Asn	Asn	Val	Lys	Pro	Val
225					230				235						240
Gln	Pro	Lys	Pro	Ala	Gln	Pro	Lys	Thr	Pro	Thr	Glu	Gln	Thr	Lys	Pro
				245					250					255	
Val	Gln	Pro	Lys	Val	Glu	Lys	Val	Lys	Pro	Thr	Val	Thr	Thr	Thr	Ser
			260					265					270		
Lys	Val	Glu	Asp	Asn	His	Ser	Thr	Lys	Val	Val	Ser	Thr	Asp	Thr	Thr
		275					280					285			
Lys	Asp	Gln	Thr	Lys	Thr	Gln	Thr	Ala	His	Thr	Val	Lys	Thr	Ala	Gln
	290					295					300				
Thr	Ala	Gln	Glu	Gln	Asn	Lys	Val	Gln	Thr	Pro	Val	Lys	Asp	Val	Ala
305					310					315					320
Thr	Ala	Lys	Ser	Glu	Ser	Asn	Asn	Gln	Ala	Val	Ser	Asp	Asn	Lys	Ser
				325					330					335	
Gln	Gln	Thr	Asn	Lys	Val	Thr	Lys	His	Asn	Glu	Thr	Pro	Lys	Gln	Ala
			340					345					350		
Ser	Lys	Ala	Lys	Glu	Leu	Pro	Lys	Thr	Gly	Leu	Thr	Ser	Val	Asp	Asn
	355					360						365			
Phe	Ile	Ser	Thr	Val	Ala	Phe	Ala	Thr	Leu	Ala	Leu	Leu	Gly	Ser	Leu
	370					375					380				
Ser	Leu	Leu	Leu	Phe	Lys	Arg	Lys	Glu	Ser	Lys					
385					390					395					

<210> 7

<211> 350

<212> PRT

<213> S. aureus

<400> 7

Met	Thr	Lys	His	Tyr	Leu	Asn	Ser	Lys	Tyr	Gln	Ser	Glu	Gln	Arg	Ser
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Ser	Ala	Met	Lys	Ile	Thr	Met	Gly	Thr	Ala	Ser	Ile	Ile	Leu	Gly	
		20					25					30			
Ser	Leu	Val	Tyr	Ile	Gly	Ala	Asp	Ser	Gln	Gln	Val	Asn	Ala	Ala	Thr
	35					40					45				
Glu	Ala	Thr	Asn	Ala	Thr	Asn	Asn	Gln	Ser	Thr	Gln	Val	Ser	Gln	Ala
	50					55					60				
Thr	Ser	Gln	Pro	Ile	Asn	Phe	Gln	Val	Gln	Lys	Asp	Gly	Ser	Ser	Glu
65					70					75					80
Lys	Ser	His	Met	Asp	Asp	Tyr	Met	Gln	His	Pro	Gly	Lys	Val	Ile	Lys
			85						90					95	
Gln	Asn	Asn	Lys	Tyr	Tyr	Phe	Gln	Thr	Val	Leu	Asn	Asn	Ala	Ser	Phe
		100						105					110		
Trp	Lys	Glu	Tyr	Lys	Phe	Tyr	Asn	Ala	Asn	Asn	Gln	Glu	Leu	Ala	Thr
		115					120					125			
Thr	Val	Val	Asn	Asp	Asn	Lys	Lys	Ala	Asp	Thr	Arg	Thr	Ile	Asn	Val
	130					135					140				
Ala	Val	Glu	Pro	Gly	Tyr	Lys	Ser	Leu	Thr	Thr	Lys	Val	His	Ile	Val
145					150					155					160
Val	Pro	Gln	Ile	Asn	Tyr	Asn	His	Arg	Tyr	Thr	Thr	His	Leu	Glu	Phe

				165				170				175			
Glu	Lys	Ala	Ile	Pro	Thr	Leu	Ala	Asp	Ala	Ala	Lys	Pro	Asn	Asn	Val
				180				185				190			
Lys	Pro	Val	Gln	Pro	Lys	Pro	Ala	Gln	Pro	Lys	Thr	Pro	Thr	Glu	Gln
				195				200				205			
Thr	Lys	Pro	Val	Gln	Pro	Lys	Val	Glu	Lys	Val	Lys	Pro	Thr	Val	Thr
				210				215				220			
Thr	Thr	Ser	Lys	Val	Glu	Asp	Asn	His	Ser	Thr	Lys	Val	Val	Ser	Thr
225				230				235				240			
Asp	Thr	Thr	Lys	Asp	Gln	Thr	Lys	Thr	Gln	Thr	Ala	His	Thr	Val	Lys
				245				250				255			
Thr	Ala	Gln	Thr	Ala	Gln	Glu	Gln	Asn	Lys	Val	Gln	Thr	Pro	Val	Lys
				260				265				270			
Asp	Val	Ala	Thr	Ala	Lys	Ser	Glu	Ser	Asn	Asn	Gln	Al			